

# Model equations

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An abbreviated version of this protocol was published in eLIFE in Nov 2016

Structure in the variability of the basic reproductive number ( $R_0$ ) for Zika epidemics in the Pacific islands

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## Detailed protocol

The calculations are detailed in the method section, in the paragraph called "R0 calculation". The methodology is well detailed in quantitative epidemiology textbooks and well-explained examples can be found in

1. P. van den Driessche & J. Watmough, "Reproduction numbers and sub-threshold endemic equilibrium for compartmental models of disease transmission", Mathematical Biosciences 2002
2. P. van den Driessche, "Reproduction numbers of infectious disease models", Infectious disease modelling, 2017

**How to cite:** (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Champagne, C. (2020). Model equations. Bio-protocol Preprint. [bio-protocol.org/prep294](https://bio-protocol.org/prep294).
2. Champagne, C., Salthouse, D. G., Paul, R., Cao-Lormeau, V., Roche, B. and Cazelles, B. (2016). Structure in the variability of the basic reproductive number ( $R_0$ ) for Zika epidemics in the Pacific islands. eLIFE. DOI: [10.7554/eLife.19874](https://doi.org/10.7554/eLife.19874)

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